Amendments to the Specification

Please replace the paragraph beginning at page 5, line 18, with the following amended paragraph.

TABLE 2: Residues within about 4Å of the FAD binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1).

Please replace the paragraph beginning at page 6, line 1, with the following amended paragraph.

TABLE 3: Residues within about 7Å of the FAD binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1).

Please replace the paragraph beginning at page 7, line 1, with the following amended paragraph.

TABLE 4: Residues within about 10Å of the FAD binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1).

Please replace the paragraph beginning at page 8, line 1, with the following amended paragraph.

TABLE 5: Residues within about 4Å of Cys135-Cys 138 at the active site (SEQ ID NO:1).

Please replace the paragraph beginning at page 8, line 4, with the following amended paragraph.

TABLE 6: Residues within about 7Å of Cys135-Cys 138 at the active site (SEQ ID NO:1).

Please replace the paragraph beginning at page 8, line 7, with the following amended paragraph.

TABLE 7: Residues within about 10Å of Cys135-Cys 138 at the active site (SEQ ID NO:1).

Please replace the paragraph beginning at page 10, line 16, with the following amended paragraph.

Figure 5 illustrates electron density maps from multiple anomalous dispersion phases with a portion of the final model refined against the second data set. Figures 5a and 5b illustrate electron density maps for the first data set before solvent flattening (Figure 5a) and after solvent flattening (Figure 5b). Figures 5c and 5d illustrate electron density maps for the second data set before solvent flattening (Figure 5c) and after solvent flattening (Figure 5d). ~~Figure 6 illustrates electron density maps from multiple anomalous dispersion phases showing a helix. Figures 6a and 6b illustrate electron density maps for the first data set before solvent flattening (Figure 6a) and after solvent flattening (Figure 6b). Figures 6c and 6d illustrate electron density maps for the second data set before solvent flattening (Figure 6c) and after solvent flattening (Figure 6d). While both maps clearly show the secondary structure, the maps illustrated in Figures 6c and 6d are clearer.~~

Please insert the following new paragraph at page 11, immediately after line 6.

Figure 6 illustrates electron density maps from multiple anomalous dispersion phases. Figures 6a and 6b illustrate electron density maps for the first data set before solvent flattening (Figure 6a) and after solvent flattening (Figure 6b). Figures 6c and 6d illustrate electron density maps for the second data set before solvent flattening (Figure 6c) and after solvent flattening (Figure 6d).

Please replace the paragraph beginning at page 11, line 16, with the following amended paragraph.

Figure 10 illustrates a stereoview of the superposition of all corresponding residues (r.m.s.d. 2.12Å) between *E. coli* thioredoxin reductase (SEQ ID NO:2) (light residues 5-54, 59-190, 198-224, 229-255, 261-266, 274-316) and *S. aureus* thioredoxin reductase (SEQ ID NO:1) (dark; residues 6-55, 59-190, 195-221, 225-251, 258-263, 266-308).

Please replace the paragraph beginning at page 11, line 24, with the following amended paragraph.

Figure 12 illustrates a stereoview of the superposition of residues in domain 1 (r.m.s.d. 1.47Å) between *E. coli* thioredoxin reductase (SEQ ID NO:2) (light; residues 5-54, 59-116, 246-255, 261-266, 274-316) and *S. aureus* [[)]] thioredoxin reductase (SEQ ID NO:1) (dark; residues 6-55, 59-116, 242-251, 258-263, 266-308).

Please replace the paragraph beginning at page 11, line 28 with the following amended paragraph.

Figure 13 illustrates a stereoview of the superposition of residues in domain 2 (r.m.s.d. 1.12Å) between *E. coli* thioredoxin reductase (SEQ ID NO:2) (light; residues 117-190, 198-224, 229-245) and *S. aureus*[[)]] thioredoxin reductase (SEQ ID NO:1) (dark; residues 117-190, 195-221, 225-241).

Please replace the paragraph beginning at page 12, line 1, with the following amended paragraph.

Figure 14 illustrates a stereoview of the superposition of all corresponding residues (r.m.s.d. 1.41Å) between *A. thaliana* thioredoxin reductase (SEQ ID NO:2) (light; residues 6-35, 39-55, 58-124, 130-141, 145-204, 217-253, 276-316) and *S. aureus* [[)]] thioredoxin reductase (SEQ ID NO:1) (dark; residues 7-36, 40-56, 58-124, 130-141, 145-204, 213-249, 268-308).

Please replace the paragraph beginning at page 12, line 9, with the following amended paragraph.

Figure 16 illustrates a stereoview of the superposition of domain 1 residues (r.m.s.d. 1.12Å) between *A. thaliana* thioredoxin reductase (SEQ ID NO:3) (light; residues 6-35, 39-55, 58-116, 246-253, 276-316) and *S. aureus* [[)]] thioredoxin reductase (SEQ ID NO:1) (dark; residues 7-36, 40-56, 58-116, 242-249, 268-308).

Please replace the paragraph beginning at page 12, line 13, with the following amended paragraph.

Figure 17 illustrates a stereoview of the superposition of domain 2 residues (r.m.s.d. 0.86Å) between *A. thaliana* thioredoxin reductase (SEQ ID NO:3) (light; residues 117-124, 130-141, 145-204, 217-245) and *S. aureus* [[)]] thioredoxin reductase (SEQ ID NO:1) (dark; residues 117-124, 130-141, 145-204, 213-241).

Please replace the paragraph beginning at page 17, line 15, with the following amended paragraph.

The FAD binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1) is located in domain 1, and preferably includes the amino acids listed in Table 2, more preferably the amino acids listed in Table 3, and most preferably the amino acids listed in Table 4, as represented by the structure coordinates listed in Table 1. It will be readily apparent to those of skill in the art that the numbering of amino acids in other isoforms of *S. aureus* thioredoxin reductase may be different than that of recombinant *S. aureus* thioredoxin reductase expressed in *E. coli*. Alternatively, the FAD binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1) includes those amino acids whose backbone atoms are situated within about 4Å, more preferably within about 7Å, most preferably within about 10Å, of one or more constituent atoms of a bound FAD cofactor or analog, as determined from the structure coordinates listed in Table 1.

Please replace the paragraph beginning at page 17, line 27, with the following amended paragraph.

The putative NADPH binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1) is located in domain 2 and includes Cys 135, Cys 138, and preferably the amino acids listed in Table 5, more preferably the amino acids listed in Table 6, and most preferably the amino acids listed in Table 7, as represented by the structure coordinates listed in Table 1. Alternatively, the putative NADPH binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1) includes those amino acids whose backbone atoms are situated within about 4Å, more preferably within about 7Å, most preferably within about 10Å, of one or more constituent atoms of a bound ligand, as determined from the structure coordinates listed in Table 1.

Please replace the paragraph beginning at page 19, line 22, with the following amended paragraph.

In one embodiment, the scalable three-dimensional configuration includes points derived from structure coordinates representing the locations of the backbone atoms of a plurality of amino acids defining the *S. aureus* thioredoxin reductase (SEQ ID NO:1) FAD binding site, preferably the amino acids listed is Table 2, more preferably the amino acids listed in Table 3, and most preferably the amino acids listed in Table 4; in another embodiment, the three-dimensional configuration includes points derived from structure coordinates representing the locations of the side chain and the backbone atoms (other than hydrogens) of a plurality of the amino acids defining the *S. aureus* thioredoxin reductase (SEQ ID NO:1) FAD binding site, preferably the amino acids listed is Table 2, more preferably the amino acids listed in Table 3, and most preferably the amino acids listed in Table 4.

Please replace the paragraph beginning at page 20, line 3, with the following amended paragraph.

In another embodiment, the scalable three-dimensional configuration includes points derived from structure coordinates representing the locations of the backbone atoms of a plurality of amino acids defining an NADPH binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1), the amino acids including Cys 135, Cys 138, and preferably the amino acids listed is Table 5, more preferably the amino acids listed in Table 6, and most preferably the amino acids listed in Table 7; in another embodiment, the three-dimensional configuration includes points derived from structure coordinates representing the locations of the side chain and the backbone atoms (other than hydrogens) of a plurality of the amino acids defining an NADPH binding site of *S. aureus* thioredoxin reductase (SEQ ID NO:1), the amino acids including Cys 135, Cys 138, and preferably the amino acids listed in Table 5, more preferably the amino acids listed in Table 6, and most preferably the amino acids listed in Table 7.

Please replace the paragraph beginning at page 41, line 5, with the following amended paragraph.

Purified *S. aureus* thioredoxin reductase was screened for crystallization conditions using reagent kits available under the trade designations HAMPTON CRYSTAL SCREEN ~~Hampton Crystal Screen~~ I and II (available from Hampton Research, Laguna Niguel, CA) and WIZARD SCREEN ~~Wizard Screen~~ I and II (available from Emerald Biostructures, Inc., Bainbridge Island, WA). Several hits were obtained in first round screening that were comprised of small yellow crystals. The most promising condition, using the reagent kit available under the trade designation HAMPTON SCREEN ~~Hampton Screen~~ I condition number 33 (4M Sodium Formate), was explored using a follow-up screen to test the effect of decreasing concentrations of sodium formate on crystal formation. Optimal crystal growth was obtained between 3.2M and 3.6M sodium formate. The size and reproducibility of crystal formation was enhanced by elimination of the nonspecific protein precipitate and by streak seeding as described in the Materials and Methods. Selenomethionine *S. aureus* thioredoxin reductase was also prepared

and crystallized to facilitate structure determination. A fluorescence scan near the K edge of selenium for the selenomethionine *S. aureus* thioredoxin reductase was recorded.

Please replace the paragraph beginning at page 44, line 12, with the following amended paragraph.

The sample was delivered in 50 mM Tris, 1 mM EDTA, pH 8.0 for crystallization screening. Protein concentration was measured using the absorbance at 454 nm. *S. aureus* thioredoxin reductase was concentrated to 15 mg/mL using a an Ultra-Free 4 concentrator with a 10,000 Da molecular weight cutoff available from Millipore (Bedford, MA). Initial screening for crystallization conditions was conducted using reagent kits available under the trade designations HAMPTON CRYSTAL SCREEN ~~Hampton Crystal Screen~~ I (available from Hampton Research, Laguna Niguel, CA) and WIZARD SCREEN ~~Wizard Screen~~ I (available from Emerald Biostructures, Inc., Bainbridge Island, WA). Crystals or microcrystals were obtained in conditions 4, 16, 29, 33, and 38 of the reagent kit available under the trade designation HAMPTON CRYSTAL SCREEN ~~Hampton Crystal Screen~~ I and conditions 6, 14, 18, 29, 34, 36 of the reagent kit available under the trade designation WIZARD SCREEN ~~Wizard Screen~~ I. Reagent kits avilable under the trade designations CRYO SCREENS ~~Cryo Screens~~ I and II (available from Emerald Biostructures, Inc., Bainbridge Island, WA) were also tested without success. A follow-up screen for ~~Hampton Crystal Screen I~~ condition 33 of the reagent kit available under the trade designation HAMPTON CRYSTAL SCREEN I (4M sodium formate) was conducted by varying sodium formate and protein concentrations. Crystals grew over a period of 1 to 3 days. Cryogenic solution conditions were obtained by transferring the crystals to 4M sodium formate just prior to freezing.